



9/30

## **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/045,574  
Source: O/P  
Date Processed by STIC: 10/03/02

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)**
- 2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202**
- 3. Hand Carry directly to:**  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
- 4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202**

Revised 01/29/2002

NOT AVAILABLE COPY

# Raw Sequence Listing Error Summary

01PE

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 101045,574

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☒ Wrapped Nucleics  
Wrapped Aminos  
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ Invalid Line Length  
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☒ Misaligned Amino  
Numbering  
The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ Non-ASCII  
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ Variable Length  
Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0  
"bug"  
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ Skipped Sequences  
(OLD RULES)  
Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ Skipped Sequences  
(NEW RULES)  
Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9 ☐ Use of n's or Xaa's  
(NEW RULES)  
Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 ☐ Invalid <213>  
Response  
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ Use of <220>  
Sequence(s) \_\_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0  
"bug"  
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ Misuse of n  
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



Does Not Comply  
Corrected Diskette Needed

OIPE

## RAW SEQUENCE LISTING

DATE: 10/03/2002

PATENT APPLICATION: US/10/045,574

TIME: 14:09:42

Input Set : A:\EP.txt

Output Set: N:\CRF4\10032002\J045574.raw

4 <110> APPLICANT: BIOGEN, INC.  
5 MACKAY, Fabienne  
6 KALLED, Susan  
9 <120> TITLE OF INVENTION: BAFF, Inhibitors Thereof and Their Use  
10 in the Modulation of B-Cell Response and Treatment of  
11 Autoimmune Disorders  
13 <130> FILE REFERENCE: A070 US CP  
15 <140> CURRENT APPLICATION NUMBER: 10/045,574  
16 <141> CURRENT FILING DATE: 2001-11-07  
18 <150> PRIOR APPLICATION NUMBER: 60/117,169  
19 <151> PRIOR FILING DATE: 1999-01-25  
21 <150> PRIOR APPLICATION NUMBER: 60/143,228  
22 <151> PRIOR FILING DATE: 1999-07-09  
24 <150> PRIOR APPLICATION NUMBER: PCT/US00/01788  
25 <151> PRIOR FILING DATE: 2000-01-25  
27 <150> PRIOR APPLICATION NUMBER: 09/911,777  
28 <151> PRIOR FILING DATE: 2001-07-24  
30 <160> NUMBER OF SEQ ID NOS: 22  
32 <170> SOFTWARE: FastSEQ for Windows Version 4.0

The type of errors shown exist throughout  
the Sequence Listing. Please check subsequent  
sequences for similar errors.

## ERRORED SEQUENCES

34 <210> SEQ ID NO: 1  
35 <211> LENGTH: 218  
36 <212> TYPE: PRT  
37 <213> ORGANISM: Homo Sapien  
39 <400> SEQUENCE: 1  
40 Met Asp Asp Ser Thr Glu Arg Glu Gln Ser Arg Leu Thr Ser Cys Leu 1  
E--> 41 5 10 15 Lys Lys Arg Glu Glu Met Lys Leu  
42 Lys Glu Cys Val Ser Ile Leu Pro 20 25  
E--> 43 30 Arg Lys Glu Ser Pro Ser Val Leu Leu Ser Cys Cys Leu Thr Val Val  
E--> 44 35 40 45 Ser Phe Tyr Gln Val Ala  
45 Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg 50 55  
E--> 46 60 Ala Glu Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala  
E--> 47 Lys65 70 75 80 Ile Phe Glu  
48 Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn Ser 85  
E--> 49 90 95 Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Val  
E--> 50 Thr Gln Asp 100 105 110 Cys  
51 Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys Gly 115  
E--> 52 120 125 Ser Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe  
53 Lys Arg Gly Ser Ala 130 135 140  
54 Leu Tyr Gly Gln Val Leu Tyr Thr Asp Lys Thr Tyr Ala Met Gly His145

*Amino numbers misaligned; wrapped amino  
- See error summary sheet,  
items 1+3*

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Input Set : A:\EP.txt

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```

E--> 55 150          155          160 Leu Ile Gln Arg Lys Lys Val His Val
      56 Phe Gly Asp Glu Leu Ser Leu          165          170
E--> 57 175          Val Thr Leu Phe Arg Cys Ile Gln Asn Leu Glu Glu Gly Asp Glu Leu
E--> 58 180          185          190          Gln Leu Ala Ile Pro Arg Glu
      59 Asn Ala Gln Ile Ser Leu Asp Gly Asp          195          200
      60 205          Val Thr Phe Phe Gly Ala Leu Lys Leu Leu          210
E--> 61 215
      63 <210> SEQ ID NO: 2
      64 <211> LENGTH: 232
      65 <212> TYPE: PRT
      66 <213> ORGANISM: Murine
      68 <400> SEQUENCE: 2
      69 Met Asp Glu Ser Ala Lys Thr Leu Pro Pro Pro Cys Leu Cys Phe Cys 1
E--> 70 5          10          15          Ser Glu Lys Gly Glu Asp Met Lys
      71 Val Gly Tyr Asp Pro Ile Thr Pro          20          25
E--> 72 30          Gln Lys Glu Glu Gly Ala Val Leu Leu Ser Ser Ser Phe Thr Ala Met
E--> 73 35          40          45          Ser Leu Tyr Gln Leu Ala
      74 Ala Leu Gln Ala Asp Leu Met Asn Leu Arg          50          55
E--> 75 60          Met Glu Leu Gln Ser Tyr Arg Gly Ser Ala Thr Pro Ala Ala Ala
E--> 76 Lys65          70          75          80 Leu Leu Thr
      77 Pro Ala Ala Pro Arg Pro His Asn Ser Ser Arg Gly His          85
E--> 78 90          95          Arg Asn Arg Arg Ala Phe Pro Gly Pro Glu Glu Thr Glu
E--> 79 Gln Asp Val          100          105          110          Asp
      80 Leu Ser Ala Pro Pro Ala Leu Arg Asn Ile Ile Gln Asp Cys Leu          115
E--> 81 120          125          Gln Leu Ile Ala Asp Ser Asp Thr Pro Thr Ile
      82 Arg Lys Gly Thr Tyr          130          135          140
      83 Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Asn Ala Leu Tyr145
E--> 84 150          155          160 Ser Gln Val Leu Tyr Thr Asp Pro Ile
      85 Phe Ala Met Gly His Val Ile          165          170
E--> 86 175          Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu Val Thr
E--> 87 180          185          190          Leu Phe Arg Cys Ile Gln Asn
      88 Leu Glu Glu Gly Asp Glu Ile Gln Leu          195          200
E--> 89 205          Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Arg Asn Gly Asp Asp Thr
E--> 90 210          215          220          Phe Phe Gly Ala Leu
E--> 91 Lys Leu Leu225          230
      93 <210> SEQ ID NO: 3
      94 <211> LENGTH: 102
      95 <212> TYPE: PRT
      96 <213> ORGANISM: Homo Sapien
      98 <400> SEQUENCE: 3
      99 Val Thr Gln Asp Cys Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr 1
E--> 100 5          10          15          Ile Gln Lys Gly Ser Tyr Thr Phe
      101 Val Pro Trp Leu Leu Ser Phe Lys          20          25
E--> 102 30          Arg Gly Ser Ala Leu Glu Glu Lys Tyr Gly Gln Val Leu Tyr Thr Asp
E--> 103 35          40          45          Lys Thr Tyr Ala Met Gly
      104 His Leu Ile Gln Arg Lys Lys Val His Val          50          55
E--> 105 60          Phe Gly Asp Glu Leu Ser Asn Asn Ser Cys Tyr Ser Ala Gly Ile
E--> 106 Ala65          70          75          80 Lys Leu Glu
      107 Glu Gly Asp Glu Leu Gln Leu Ala Ile Pro Arg Glu Asn          85

```

## RAW SEQUENCE LISTING

DATE: 10/03/2002

PATENT APPLICATION: US/10/045,574

TIME: 14:09:42

Input Set : A:\EP.txt

Output Set: N:\CRF4\10032002\J045574.raw

```

E--> 108 90          95      Ala Gln Ile Ser Leu Asp          100
110 <210> SEQ ID NO: 4
111 <211> LENGTH: 96
112 <212> TYPE: PRT
113 <213> ORGANISM: Homo Sapien
115 <400> SEQUENCE: 4
116 Lys Gln His Ser Val Leu His Leu Val Pro Ile Asn Ala Thr Ser Lys 1
E--> 117 5          10          15      Asp Asp Ser Asp Val Thr Glu Val
118 Met Trp Gln Pro Ala Leu Arg Arg          20          25
E--> 119 30          Gly Arg Gly Leu Gln Ala Gln Tyr Ser Gln Val Leu Phe Gln Asp Val
E--> 120 35          40          45          Thr Phe Thr Met Gly Gln
121 Val Val Ser Arg Glu Gly Gln Gly Arg Ala          50          55
E--> 122 60          Tyr Asn Ser Cys Tyr Ser Ala Gly Val Phe His Leu His Gln Gly
E--> 123 Asp65          70          75          80 Ile Leu Ser
124 Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn Leu Ser          85
E--> 125 90          95
127 <210> SEQ ID NO: 5
128 <211> LENGTH: 104
129 <212> TYPE: PRT
130 <213> ORGANISM: Homo Sapien
132 <400> SEQUENCE: 5
133 Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly 1
E--> 134 5          10          15      Gln Leu Gln Trp Leu Asn Arg Arg
135 Ala Asn Ala Leu Leu Ala Asn Gly          20          25
E--> 136 30          Val Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His
E--> 137 35          40          45          Val Leu Leu Thr His Thr
138 Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr          50          55
E--> 139 60          Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly
E--> 140 Gly65          70          75          80 Val Phe Gln
141 Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg          85
E--> 142 90          95      Pro Asp Tyr Leu Asp Phe Ala Glu          100
144 <210> SEQ ID NO: 6
145 <211> LENGTH: 97
146 <212> TYPE: PRT
147 <213> ORGANISM: Homo Sapien
149 <400> SEQUENCE: 6
150 Glu Leu Arg Lys Val Ala His Leu Thr Gly Lys Ser Asn Ser Arg Ser 1
E--> 151 5          10          15      Met Pro Leu Glu Trp Glu Asp Thr
152 Tyr Gly Ile Val Leu Leu Ser Gly          20          25
E--> 153 30          Val Lys Tyr Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn Leu
E--> 154 35          40          45          Pro Leu Ser His Lys Val
155 Tyr Met Arg Asn Ser Lys Tyr Pro Gln Met          50          55
E--> 156 60          Trp Ala Arg Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr Ser
E--> 157 Ala65          70          75          80 Asp His Leu
158 Tyr Val Asn Val Ser Glu Leu Ser Leu Val Asn Phe Glu          85
E--> 159 90          95      Glu
161 <210> SEQ ID NO: 7
162 <211> LENGTH: 102
163 <212> TYPE: PRT

```

## RAW SEQUENCE LISTING

DATE: 10/03/2002

PATENT APPLICATION: US/10/045,574

TIME: 14:09:42

Input Set : A:\EP.txt

Output Set: N:\CRF4\10032002\J045574.raw

```

164 <213> ORGANISM: Homo Sapien
166 <400> SEQUENCE: 7
167 Thr Leu Lys Pro Ala Ala His Leu Ile Gly Asp Pro Ser Lys Gln Asn 1
E--> 168 5          10          15          Ser Leu Leu Trp Arg Ala Asn Thr
169 Asp Arg Ala Phe Leu Gln Asp Gly          20          25
E--> 170 30          Phe Tyr Ser Gln Val Val Phe Ser Gly Lys Ala Tyr Ser Pro Lys Ala
E--> 171 35          40          45          Thr Ser Ser Pro Leu Tyr
172 Leu Ala His Glu Val Gln Leu Phe Ser Ser          50          55
E--> 173 60          Gln Tyr Pro Phe Pro Trp Leu His Ser Met Tyr His Gly Ala Ala
E--> 174 Phe65          70          75          80 Gln Leu Thr
175 Gln Gly Asp Gln Leu Ser Thr His Thr Asp Gly Ile Pro          85
E--> 176 90          95          His Leu Val Leu Ser Phe          100
178 <210> SEQ ID NO: 8
179 <211> LENGTH: 109
180 <212> TYPE: PRT
181 <213> ORGANISM: Homo Sapien
183 <400> SEQUENCE: 8
184 Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro 1
E--> 185 5          10          15          Ser Gly Ser His Lys Val Ser Leu
186 Ser Ser Trp Tyr His Asp Arg Gly          20          25
E--> 187 30          Trp Gly Lys Ile Ser Asn Met Tyr Ala Asn Ile Cys Phe Arg His His
E--> 188 35          40          45          Glu Thr Ser Gly Asp Leu
189 Ala Thr Glu Tyr Leu Gln Leu Met Val Tyr          50          55
E--> 190 60          Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Glu Phe His Phe Tyr
E--> 191 Ser65          70          75          80 Ile Asn Val
192 Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu Ile Ser          85
E--> 193 90          95          Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln
E--> 194 100          105

```

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/045,574

DATE: 10/03/2002  
TIME: 14:09:43

Input Set : A:\EP.txt  
Output Set: N:\CRF4\10032002\J045574.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 40,42,43,44,45,46,48,49,51,52,53,54,55,56,57,58,59  
Seq#:2; Line(s) 69,71,72,73,74,75,77,78,80,81,82,83,84,85,86,87,88,89,90  
Seq#:3; Line(s) 99,101,102,103,104,105,107  
Seq#:4; Line(s) 116,118,119,120,121,122,124  
Seq#:5; Line(s) 133,135,136,137,138,139,141,142  
Seq#:6; Line(s) 150,152,153,154,155,156,158  
Seq#:7; Line(s) 167,169,170,171,172,173,175  
Seq#:8; Line(s) 184,186,187,188,189,190,192,193

## VERIFICATION SUMMARY

DATE: 10/03/2002

PATENT APPLICATION: US/10/045,574

TIME: 14:09:43

Input Set : A:\EP.txt

Output Set: N:\CRF4\10032002\J045574.raw

L:41 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 L:43 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1  
 L:43 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 M:332 Repeated in SeqNo=1  
 L:44 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 L:46 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 L:47 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 L:47 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1  
 L:49 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 L:61 M:252 E: No. of Seq. differs, <211> LENGTH:Input:218 Found:109 SEQ:1  
 L:70 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 L:72 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2  
 L:72 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 M:332 Repeated in SeqNo=2  
 L:73 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 L:75 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 L:76 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 L:76 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1  
 L:78 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 L:91 M:252 E: No. of Seq. differs, <211> LENGTH:Input:232 Found:130 SEQ:2  
 L:100 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 L:102 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3  
 L:102 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 M:332 Repeated in SeqNo=3  
 L:103 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 L:105 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 L:106 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 L:106 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1  
 L:108 M:252 E: No. of Seq. differs, <211> LENGTH:Input:102 Found:49 SEQ:3  
 L:117 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 L:119 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4  
 L:119 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 M:332 Repeated in SeqNo=4  
 L:120 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 L:122 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 L:123 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 L:123 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1  
 L:125 M:252 E: No. of Seq. differs, <211> LENGTH:Input:96 Found:49 SEQ:4  
 L:134 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 L:136 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5  
 L:136 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 M:332 Repeated in SeqNo=5  
 L:137 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 L:139 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 L:140 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 L:140 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1  
 L:142 M:252 E: No. of Seq. differs, <211> LENGTH:Input:104 Found:49 SEQ:5  
 L:151 M:333 E: Wrong sequence grouping, Amino acids not in groups!



## VERIFICATION SUMMARY

DATE: 10/03/2002

PATENT APPLICATION: US/10/045,574

TIME: 14:09:43

Input Set : A:\EP.txt

Output Set: N:\CRF4\10032002\J045574.raw

L:153 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6  
L:153 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
M:332 Repeated in SeqNo=6  
L:154 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:156 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:157 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:157 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1  
L:159 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:159 M:252 E: No. of Seq. differs, <211> LENGTH:Input:97 Found:50 SEQ:6  
L:168 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:170 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7  
L:170 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
M:332 Repeated in SeqNo=7  
L:171 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:173 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:174 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:174 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1  
L:176 M:252 E: No. of Seq. differs, <211> LENGTH:Input:102 Found:49 SEQ:7  
L:185 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:187 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8  
L:187 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
M:332 Repeated in SeqNo=8  
L:188 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:190 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:191 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:191 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1  
L:193 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:194 M:252 E: No. of Seq. differs, <211> LENGTH:Input:109 Found:62 SEQ:8